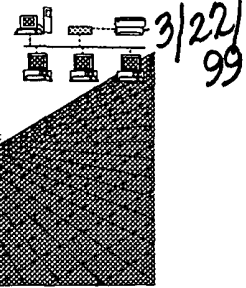


4-in 3-1/2 in

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/866 279

Art Unit / Team No. : 1632

Date Processed by STIC: 3/22/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

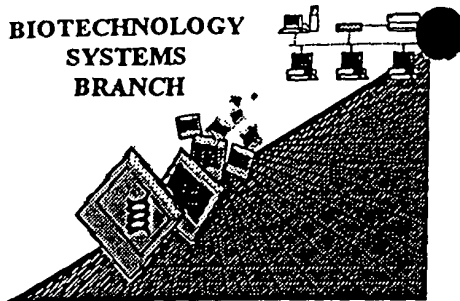
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825).

Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: [pub/checker/](ftp://ftp.uspto.gov/pub/checker/)
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

COST FOR DISKETTE IS \$ 25.00

METHOD OF PAYMENT:

Check payable to Commissioner of Patents and Trademarks

VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737

PTO Deposit Account

For Further Information, Contact: Arti Shah at 703-308-4212

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/866,279DATE: 03/22/1999
TIME: 13:44:37

INPUT SET: S31118.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: Susan DYMECKI
5 (ii) TITLE OF INVENTION: Use of Flp Recombinase in Mice
6 (iii) NUMBER OF SEQUENCES: 23
7 (iv) CORRESPONDENCE ADDRESS:
8 (A) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
9 (B) STREET: 1100 New York Avenue, N.W.
10 (C) CITY: Washington
11 (D) STATE: D.C.
12 (E) COUNTRY: USA
13 (F) ZIP: 20005-3918
14 (v) COMPUTER READABLE FORM:
15 (A) MEDIUM TYPE: Floppy disk
16 (B) COMPUTER: IBM PC compatible
17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
18 (D) SOFTWARE: Microsoft Word
19 (vi) CURRENT APPLICATION DATA:
20 (A) APPLICATION NUMBER:
21 (B) FILING DATE:
22 (C) CLASSIFICATION:
23

ERRORED SEQUENCES FOLLOW:

48 (2) INFORMATION FOR SEQ ID NO:3:
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 54 base pairs
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: single
53 (D) TOPOLOGY: linear
54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
55
56 CTAGGGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC 50
57
--> 58 TTCA (100) 54
59

262 (2) INFORMATION FOR SEQ ID NO:17:
263 (i) SEQUENCE CHARACTERISTICS:
--> 264 (A) LENGTH: 423 amino acids (P3)

RAW SEQUENCE LISTING PATENT APPLICATION US/08/866,279

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265 (B) TYPE: amino acid
 266 (C) STRANDEDNESS: single
 267 (D) TOPOLOGY: linear
 268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
 269
 270 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu
 271 1 5 10 15
 272
 273 Val Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys
 274 20 25 30
 275
 276 Ile Ala Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile
 277 35 40 45
 278
 279 Thr His Asn Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr
 280 50 55 60
 281
 282 Asn Thr Ile Ile Ser Asn Ser Leu Ser Leu Asp Ile Val Asn Lys
 283 65 70 75
 284
 285 Ser Leu Gln Phe Lys Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu
 286 80 85 90
 287
 288 Ala Ser Leu Lys Lys Leu Ile Pro Ala Trp Glu Phe Thr Ile Ile
 289 95 100 105
 290
 291 Pro Tyr Tyr Gly Gln Lys His Gln Ser Asp Ile Thr Asp Ile Val
 292 110 115 120
 293
 294 Ser Ser Leu Gln Leu Gln Phe Glu Ser Ser Glu Glu Ala Asp Lys
 295 125 130 135
 296
 297 Gly Asn Ser His Ser Lys Lys Met Leu Lys Ala Leu Leu Ser Glu
 298 140 145 150
 299
 300 Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys Ile Leu Asn Ser Phe
 301 155 160 165
 302
 303 Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr Leu Tyr Gln Phe
 304 170 175 180
 305
 306 Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe Ser Asp Ile
 307 185 190 195
 308
 309 Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr
 310 200 205 210
 311
 312 Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr Ser
 313 215 220 225
 314
 315 Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
 316 230 235 240
 317

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INPUT SET: S31118.raw

```

318 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val
319                245                250                255
320
321 Leu Lys Arg Val Asn Arg Thr Gln Asn Ser Ser Ser Asn Lys Gln
322                260                265                270
323
324 Glu Tyr Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys
325                275                280                285
326
327 Ala Leu Lys Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn
328                290                295                300
329
330 Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu
331                305                310                315
332
333 Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val Gly Asn Trp
334                320                325                330
335
336 Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr Thr His
337                335                340                345
338
--> 339 Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ala Leu Val Ser Arg
340                350                355                360
341
342 Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys
343                365                370                375
344
345 Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu
346                380                385                390
347
348 Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly
349                395                400                405
350
351 Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn
352                410                415                420
353
354 Arg Arg Ile
355

```

```

408 (2) INFORMATION FOR SEQ ID NO:19:
409 (i) SEQUENCE CHARACTERISTICS:
--> 410 (A) LENGTH: 423 amino acids
411 (B) TYPE: amino acid
412 (C) STRANDEDNESS: single
413 (D) TOPOLOGY: linear
414 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
415
416 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu
417 1 5 10 15
418
419 Val Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys
420 20 25 30
421

```

(p.5)

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TIME: 13:44:38

INPUT SET: S31118.raw

422	Ile	Ala	Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile
423					35					40					45
424															
425	Thr	His	Asn	Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr
426					50					55					60
427															
428	Asn	Thr	Ile	Ile	Ser	Asn	Ser	Leu	Ser	Phe	Asp	Ile	Val	Asn	Lys
429					65					70					75
430															
431	Ser	Leu	Gln	Phe	Lys	Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu
432					80					85					90
433															
434	Ala	Ser	Leu	Lys	Lys	Leu	Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile
435					95					100					105
436															
437	Pro	Tyr	Tyr	Gly	Gln	Lys	His	Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val
438					110					115					120
439															
440	Ser	Ser	Leu	Gln	Leu	Gln	Phe	Glu	Ser	Ser	Glu	Glu	Ala	Asp	Lys
441					125					130					135
442															
443	Gly	Asn	Ser	His	Ser	Lys	Lys	Met	Leu	Lys	Ala	Leu	Leu	Ser	Glu
444					140					145					150
445															
446	Gly	Glu	Ser	Ile	Trp	Glu	Ile	Thr	Glu	Lys	Ile	Leu	Asn	Ser	Phe
447					155					160					165
448															
449	Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	Leu	Tyr	Gln	Phe
450					170					175					180
451															
452	Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	Ser	Asp	Ile
453					185					190					195
454															
455	Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn	Lys	Tyr
456					200					205					210
457															
458	Leu	Gly	Val	Ile	Ile	Gln	Cys	Leu	Val	Thr	Glu	Thr	Lys	Thr	Ser
459					215					220					225
460															
461	Val	Ser	Arg	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arg	Gly	Arg	Ile	Asp
462					230					235					240
463															
464	Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val
465					245					250					255
466															
467	Leu	Lys	Arg	Val	Asn	Arg	Thr	Gln	Asn	Ser	Ser	Ser	Asn	Lys	Gln
468					260					265					270
469															
470	Glu	Tyr	Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys
471					275					280					285
472															
473	Ala	Leu	Lys	Lys	Asn	Ala	Pro	Tyr	Ser	Ile	Phe	Ala	Ile	Lys	Asn
474					290					295					300

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/866,279

DATE: 03/22/1999

TIME: 13:44:39

INPUT SET: S31118.raw

475
476 Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu
477 305 310 315
478
479 Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val Gly Asn Trp
480 320 325 330
481
482 Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr Thr His
483 335 340 345
484
--> 485 Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ale Leu Val Ser Arg
486 350 355 360
487
488 Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys
489 365 370 375
490
491 Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu
492 380 385 390
493
494 Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly
495 395 400 405
496
497 Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn
498 410 415 420
499
500 Arg Arg Ile
501

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/866,279

DATE: 03/22/1999

TIME: 13:44:39

INPUT SET: S31118.raw

Line	Error	Original Text
58	# of Sequences for line conflicts w/ running total	TTCA
264	Entered (423) and Calc. Seq. Length (422) differ	(A) LENGTH: 423 amino acids
339	Wrong Amino Acid Designator	Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ale Leu Val Ser A
410	Entered (423) and Calc. Seq. Length (422) differ	(A) LENGTH: 423 amino acids
485	Wrong Amino Acid Designator	Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ale Leu Val Ser A